

OIPE

RAW SEQUENCE LISTING

DATE: 11/01/2001

PATENT APPLICATION: US/09/977,406

TIME: 10:45:21

Input Set : A:\sequence-listing-ASCII-us-03.txt

Output Set: N:\CRF3\11012001\I977406.raw

Does Not Comply
Corrected Diskette Needed

OK 4 <110> APPLICANT: PROCYON BIOPHARMA INC.
 W--> 5 <120> TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING
 TUMORS
 W--> 6 <130> FILE REFERENCE: 06508-030-us-03
 C--> 7 <140> CURRENT APPLICATION NUMBER: US/09/977,406
 OK 7 <141> CURRENT FILING DATE: 2001-10-15
 7 <150> PRIOR APPLICATION NUMBER: 2,321,256
 8 <151> PRIOR FILING DATE: 2000-10-16
 9 <150> PRIOR APPLICATION NUMBER: 2,355,334
 10 <151> PRIOR FILING DATE: 2001-08-20
 W--> 11 <160> NUMBER OF SEQ ID: 92

ERRORED SEQUENCES

E--> 13 <210> SEQ ID NO: SEQ ID NO: 1
 E--> 39 <210> SEQ ID NO: SEQ ID NO: 2
 E--> 67 <210> SEQ ID NO: SEQ ID NO: 3
 E--> 77 <210> SEQ ID NO: SEQ ID NO: 4
 E--> 87 <210> SEQ ID NO: SEQ ID NO: 5
 E--> 97 <210> SEQ ID NO: SEQ ID NO: 6
 E--> 110 <210> SEQ ID NO: SEQ ID NO: 7
 E--> 119 <210> SEQ ID NO: SEQ ID NO: 8
 E--> 128 <210> SEQ ID NO: SEQ ID NO: 9
 E--> 147 <210> SEQ ID NO: SEQ ID NO: 10
 E--> 157 <210> SEQ ID NO: SEQ ID NO: 11
 E--> 170 <210> SEQ ID NO: SEQ ID NO: 12
 E--> 182 <210> SEQ ID NO: SEQ ID NO: 13
 E--> 195 <210> SEQ ID NO: SEQ ID NO: 14
 E--> 209 <210> SEQ ID NO: SEQ ID NO: 15
 E--> 222 <210> SEQ ID NO: SEQ ID NO: 16
 E--> 236 <210> SEQ ID NO: SEQ ID NO: 17
 E--> 249 <210> SEQ ID NO: SEQ ID NO: 18
 E--> 263 <210> SEQ ID NO: SEQ ID NO: 19
 E--> 276 <210> SEQ ID NO: SEQ ID NO: 20

see pp 4-5

1363 <211> LENGTH: 15
 1364 <212> TYPE: PRT
 W--> 1365 <213> ORGANISM: *mandatory response*
 OK 1366 <220> FEATURE: *needed*
 OK 1367 <221> NAME/KEY: Modified site
 1368 <222> LOCATION: 1
 1369 <223> OTHER INFORMATION: The residue in this position is either glutamic acid,
 asparagin, or *asparagine*
 1370 aspartic acid.

OK 1372 <220> FEATURE:
 W 1373 <221> NAME/KEY: Modified site
 1374 <222> LOCATION: 4
 1375 <223> OTHER INFORMATION: The residue in this position is either threonine, or

see p. 3

(This is sequence 89)

serine.

W--> 1377 <220> FEATURE:

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W--> 1378 <221> NAME/KEY: Modified site
1379 <222> LOCATION: 6
1380 <223> OTHER INFORMATION: The residue in this position is either glutamic acid,
asparagin or *asparagine*
1381 aspartic acid.

W--> 1383 <220> FEATURE:
W--> 1384 <221> NAME/KEY: Modified site
1385 <222> LOCATION: 8
1386 <223> OTHER INFORMATION: The residue in this position is either glutamic acid,
asparagin or
1387 aspartic acid.

W--> 1389 <220> FEATURE:
W--> 1390 <221> NAME/KEY: Modified site
1391 <222> LOCATION: 9
1392 <223> OTHER INFORMATION: The residue in this position is either threonine, or
serine.

W--> 1394 <220> FEATURE:
W--> 1395 <221> NAME/KEY: Modified site
1396 <222> LOCATION: 11
1397 <223> OTHER INFORMATION: The residue in this position is either threonine, or
serine.

W--> 1399 <220> FEATURE:
W--> 1400 <221> NAME/KEY: Modified site
1401 <222> LOCATION: 13
1402 <223> OTHER INFORMATION: The residue in this position is either tyrosine, or
phenylalanine.

W--> 1404 <220> FEATURE:
W--> 1405 <221> NAME/KEY: Modified site
1406 <222> LOCATION: 14
1407 <223> OTHER INFORMATION: The residue in this position is either glutamic acid,
asparagin or
1408 aspartic acid.

W--> 1410 <220> FEATURE:
W--> 1411 <221> NAME/KEY: Modified site
1412 <222> LOCATION: 15
1413 <223> OTHER INFORMATION: The residue in this position is either threonine, or
serine.

E--> 1415 <400> *896 insert*
W--> 1416 Xaa Trp Gln Xaa Asp Xaa Cys Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa
E--> 1417 1 5 10 15

misaligned nos.

see pp 4-5

delete - do not show any alphabetical headings when using new sequence rules format

<210> ~~SEQ ID NO:~~ 1
<211> 94
<212> PRT
<213> ← mandatory response needed (see items 10 and 11 on Error summary sheet)
<400> 1 ← insert

Ser Cys Tyr Phe Ile Pro Asn Glu Gly Val Pro Gly Asp Ser Thr Arg
1 5 10 15

(partial listing of sequence 1)

global
errors

IMPORTANT

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

09/977,406

S

delete
<210> ~~SEQ ID NO: 7~~
<211> 26
<212> DNA
<213> *← mandatory response*
<400> *7 ← insert*

GGGAAGAATT CTCATGCTAT TTCATA

26

all bases must be in lower-case letters, when using
new sequence
header format

Please correct
all sequences showing
these errors

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/977,406

DATE: 11/01/2001

TIME: 10:45:22

Input Set : A:\sequence-listing-ASCII-us-03.txt

Output Set: N:\CRF3\11012001\I977406.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier
L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:270 C: Current Application Number differs, Replaced Current Application No
L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:11 M:283 W: Missing Blank Line separator, <160> field identifier
L:13 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:16 M:201 W: Mandatory field data missing, <213> ORGANISM
L:17 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:17 M:283 W: Missing Blank Line separator, <400> field identifier
L:39 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:42 M:201 W: Mandatory field data missing, <213> ORGANISM
L:43 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:43 M:283 W: Missing Blank Line separator, <400> field identifier
L:67 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:70 M:201 W: Mandatory field data missing, <213> ORGANISM
L:71 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:71 M:283 W: Missing Blank Line separator, <400> field identifier
L:77 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:80 M:201 W: Mandatory field data missing, <213> ORGANISM
L:81 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:81 M:283 W: Missing Blank Line separator, <400> field identifier
L:87 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:90 M:201 W: Mandatory field data missing, <213> ORGANISM
L:91 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:91 M:283 W: Missing Blank Line separator, <400> field identifier
L:97 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:100 M:201 W: Mandatory field data missing, <213> ORGANISM
L:101 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:101 M:283 W: Missing Blank Line separator, <400> field identifier
L:110 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:113 M:201 W: Mandatory field data missing, <213> ORGANISM
L:114 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:114 M:283 W: Missing Blank Line separator, <400> field identifier
L:116 M:112 C: (48) String data converted to lower case,
L:119 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:122 M:201 W: Mandatory field data missing, <213> ORGANISM
L:123 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:123 M:283 W: Missing Blank Line separator, <400> field identifier
M:112 Repeated in SeqNo=0
L:128 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:131 M:201 W: Mandatory field data missing, <213> ORGANISM
L:132 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:132 M:283 W: Missing Blank Line separator, <400> field identifier
L:147 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:150 M:201 W: Mandatory field data missing, <213> ORGANISM
L:151 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:151 M:283 W: Missing Blank Line separator, <400> field identifier
L:157 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO

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Input Set : A:\sequence-listing-ASCII-us-03.txt
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L:160 M:201 W: Mandatory field data missing, <213> ORGANISM
L:161 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:161 M:283 W: Missing Blank Line separator, <400> field identifier
L:170 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:173 M:201 W: Mandatory field data missing, <213> ORGANISM
L:174 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:174 M:283 W: Missing Blank Line separator, <400> field identifier
L:182 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:185 M:201 W: Mandatory field data missing, <213> ORGANISM
L:186 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:186 M:283 W: Missing Blank Line separator, <400> field identifier
L:195 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:198 M:201 W: Mandatory field data missing, <213> ORGANISM
L:199 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:199 M:283 W: Missing Blank Line separator, <400> field identifier
L:209 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:212 M:201 W: Mandatory field data missing, <213> ORGANISM
L:213 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:213 M:283 W: Missing Blank Line separator, <400> field identifier
L:222 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:225 M:201 W: Mandatory field data missing, <213> ORGANISM
L:226 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:226 M:283 W: Missing Blank Line separator, <400> field identifier
L:236 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:239 M:201 W: Mandatory field data missing, <213> ORGANISM
L:240 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:240 M:283 W: Missing Blank Line separator, <400> field identifier
L:249 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:252 M:201 W: Mandatory field data missing, <213> ORGANISM
L:253 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:253 M:283 W: Missing Blank Line separator, <400> field identifier
L:263 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:266 M:201 W: Mandatory field data missing, <213> ORGANISM
L:267 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:267 M:283 W: Missing Blank Line separator, <400> field identifier
L:276 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:279 M:201 W: Mandatory field data missing, <213> ORGANISM
L:280 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:280 M:283 W: Missing Blank Line separator, <400> field identifier
L:289 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:292 M:201 W: Mandatory field data missing, <213> ORGANISM
L:293 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:293 M:283 W: Missing Blank Line separator, <400> field identifier
L:303 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:306 M:201 W: Mandatory field data missing, <213> ORGANISM
L:307 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:307 M:283 W: Missing Blank Line separator, <400> field identifier
L:316 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:319 M:201 W: Mandatory field data missing, <213> ORGANISM

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Input Set : A:\sequence-listing-ASCII-us-03.txt

Output Set: N:\CRF3\11012001\I977406.raw

L:320 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:320 M:283 W: Missing Blank Line separator, <400> field identifier
 L:329 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:332 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:333 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:333 M:283 W: Missing Blank Line separator, <400> field identifier
 L:343 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:346 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:347 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:347 M:283 W: Missing Blank Line separator, <400> field identifier
 L:360 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:361 M:283 W: Missing Blank Line separator, <400> field identifier
 L:373 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:374 M:283 W: Missing Blank Line separator, <400> field identifier
 L:389 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:390 M:283 W: Missing Blank Line separator, <400> field identifier
 L:405 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:406 M:283 W: Missing Blank Line separator, <400> field identifier
 L:421 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:422 M:283 W: Missing Blank Line separator, <400> field identifier
 L:437 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:438 M:283 W: Missing Blank Line separator, <400> field identifier
 L:454 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:455 M:283 W: Missing Blank Line separator, <400> field identifier
 L:471 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:472 M:283 W: Missing Blank Line separator, <400> field identifier
 L:487 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:488 M:283 W: Missing Blank Line separator, <400> field identifier
 L:504 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:505 M:283 W: Missing Blank Line separator, <400> field identifier
 L:521 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:522 M:283 W: Missing Blank Line separator, <400> field identifier
 L:537 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:538 M:283 W: Missing Blank Line separator, <400> field identifier
 L:553 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:554 M:283 W: Missing Blank Line separator, <400> field identifier
 L:569 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:570 M:283 W: Missing Blank Line separator, <400> field identifier
 L:585 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:586 M:283 W: Missing Blank Line separator, <400> field identifier
 L:601 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:602 M:283 W: Missing Blank Line separator, <400> field identifier
 L:617 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:618 M:283 W: Missing Blank Line separator, <400> field identifier
 L:633 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:634 M:283 W: Missing Blank Line separator, <400> field identifier
 L:653 M:201 W: Mandatory field data missing, <213> ORGANISM
 L:654 M:283 W: Missing Blank Line separator, <400> field identifier
 L:672 M:201 W: Mandatory field data missing, <213> ORGANISM

VERIFICATION SUMMARY

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TIME: 10:45:22

Input Set : A:\sequence-listing-ASCII-us-03.txt

Output Set: N:\CRF3\11012001\I977406.raw

L:673 M:283 W: Missing Blank Line separator, <400> field identifier
L:691 M:201 W: Mandatory field data missing, <213> ORGANISM
L:692 M:283 W: Missing Blank Line separator, <400> field identifier
L:710 M:201 W: Mandatory field data missing, <213> ORGANISM
L:711 M:283 W: Missing Blank Line separator, <400> field identifier
L:729 M:201 W: Mandatory field data missing, <213> ORGANISM
L:748 M:201 W: Mandatory field data missing, <213> ORGANISM
L:767 M:201 W: Mandatory field data missing, <213> ORGANISM
L:1367 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1373 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1378 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1384 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1390 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1395 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1400 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1405 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1411 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1416 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:1417 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

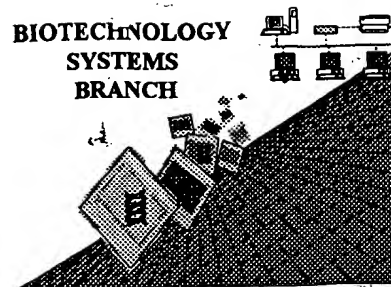
SERIAL NUMBER: 09/977,406

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOF

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response **PMI** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> **PMI** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

0590
1109



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/977,406
Source: O/P
Date Processed by STIC: 11/1/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>